IN THE SPECIFCATION

Page 12, line 5, please replace the text in its entirety with the following:

- the *sod* gene which codes for superoxide dismutase (U.S. patent no. 6,569,650 ~~US: 09/373,731~~),

Page 12, line 13, please replace the text in its entirety with the following:

- the *pgi* gene which codes for glucose 6-phosphate isomerase (~~US: 09/396,478~~ U.S. patent no. 6,586,214, DSM 12969),

Page 25 (Abstract), please replace the Abstract in its entirety with the attached substitute Abstract.

The following listing of claims will replace all prior versions, and listings of claims in this application:

1. (Original) An isolated polynucleotide, which encodes a protein comprising the amino acid sequence of SEQ ID NO:2.

Claim 2. (Cancelled)

3. (Original) A vector comprising the isolated polynucleotide of Claim 1.

4. (Original) A host cell comprising the isolated polynucleotide of Claim 1.

5. (Currently Amended) The host cell of Claim 4, which is a ~~*Coryneform* bacterium~~ *Corynebacterium*.

6. (Currently Amended) The host cell of Claim 4, wherein said host cell is selected from the group consisting of ~~*Coryneform*~~ *Corynebacterium glutamicum, Corynebacterium acetoglutamicum, Corynebacterium acetoacidophilum, Corynebacterium melassecola, Corynebacterium thermoaminogenes,* and *Brevibacterium flavum,* ~~*Brevibacterium lactofermentum,* and *Brevibacterium divaricatum*~~.

7. (Withdrawn) A method for detecting a nucleic acid with at least 70% homology to nucleotide of Claim 1, comprising contacting a nucleic acid sample with a probe or primer comprising at least 15 consecutive nucleotides of the nucleotide sequence of Claim 1, or at least 15 consecutive nucleotides of the complement thereof.

8. (Withdrawn) A method for producing a nucleic acid with at least 70% homology to nucleotide of Claim 1, comprising contacting a nucleic acid sample with a primer comprising at least 15 consecutive nucleotides of the nucleotide sequence of Claim 1, or at least 15 consecutive nucleotides of the complement thereof.

9. (Withdrawn) A process for screening for polynucleotides, which encode a protein having OxyR transcriptional regulator activity comprising

a) hybridizing the isolated polynucleotide of Claim 1 to the polynucleotide to be screened;

b) expressing the polynucleotide to produce a protein; and

c) detecting the presence or absence of OxyR transcriptional regulator activity in said protein.

10. (Original) A method for making OxyR transcriptional regulator protein, comprising

a) culturing the host cell of Claim 4 for a duration of time under conditions suitable for expression of OxyR transcriptional regulator protein; and

b) collecting the OxyR transcriptional regulator protein.

11. (Original) An isolated polynucleotide, which comprises SEQ ID NO:1.

12. (Currently Amended) An isolated polynucleotide, which is fully complimentary to the polynucleotide of Claim 11.

13. (Currently Amended) An isolated polynucleotide, which is at least 70% identical to SEQ ID NO:1 and encodes a protein with OxyR transcriptional regulator activity ~~the polynucleotide of Claim 11~~.

14. (Currently Amended) An isolated polynucleotide, which is at least 80% identical to SEQ ID NO:1 and encodes a protein with OxyR transcriptional regulator activity ~~the polynucleotide of Claim 11~~.

15. (Currently Amended) An isolated polynucleotide, which is at least 90% identical to SEQ ID NO:1 and encodes a protein with OxyR transcriptional regulator activity ~~the polynucleotide of Claim 11~~.

16. (Currently Amended) An isolated polynucleotide, ~~which comprises at least 15 consecutive nucleotides of the polynucleotide of Claim 11~~ consisting of a nucleotide sequence selected from the group consisting of at least 15 consecutive nucleotides of nucleotides 1 to 490 of SEQ ID NO:1, at least 15 consecutive nucleotides of the complement of nucleotides 1 to 490 of SEQ ID NO:1, at least 25 consecutive nucleotides of nucleotides

491 to 1471 of SEQ ID NO:1, at least 25 consecutive nucleotides of the complement of nucleotides 491 to 1471 of SEQ ID NO:1, at least 15 consecutive nucleotides of nucleotides 1472 to 1675 of SEQ ID NO:1, and at least 25 consecutive nucleotides of the complement of nucleotides 1472 to 1675 of SEQ ID NO:1

17. (Currently Amended) An isolated polynucleotide, which hybridizes under stringent conditions to SEQ ID NO: 1~~the polynucleotide of Claim 11~~; wherein said stringent conditions comprise washing in ~~5X SSC at a temperature from 50 to 68°C~~ 2 X SSC at a temperature of from 50 to 68°C which is at least 70% identical to SEQ ID NO:1, and which encodes a protein with OxyR transcriptional regulation activity.

Claim 18 (Cancelled).

19. (Original) A vector comprising the isolated polynucleotide of Claim 11.

20. (Original) A host cell comprising the isolated polynucleotide of Claim 11.

21. (Original) The host cell of Claim 20, which is a *Coryneform* bacterium.

22. (Currently Amended) The host cell of Claim 20, wherein said host cell is selected from the group consisting of ~~*Coryneform*~~ *Corynebacterium glutamicum, Corynebacterium acetoglutamicum, Corynebacterium acetoacidophilum, Corynebacterium melassecola, Corynebacterium thermoaminogenes,* and *Brevibacterium flavum,* ~~*Brevibacterium lactofermentum,* and *Brevibacterium divaricatum*~~.

23. (Withdrawn) A process for screening for polynucleotides, which encode a protein having OxyR transcriptional regulator activity comprising

a) hybridizing the isolated polynucleotide of Claim 11 to the polynucleotide to be screened;

b) expressing the polynucleotide to produce a protein; and

c) detecting the presence or absence of OxyR transcriptional regulator activity in said protein.

24. (Withdrawn) A method for detecting a nucleic acid with at least 70% homology to nucleotide of Claim 11, comprising contacting a nucleic acid sample with a probe or primer comprising at least 15 consecutive nucleotides of the nucleotide sequence of Claim 11, or at least 15 consecutive nucleotides of the complement thereof.

25. (Withdrawn) A method for producing a nucleic acid with at least 70% homology to nucleotide of Claim 11, comprising contacting a nucleic acid sample with a primer comprising at least 15 consecutive nucleotides of the nucleotide sequence of Claim 11, or at least 15 consecutive nucleotides of the complement thereof.

26. (Original) A method for making OxyR transcriptional regulator protein, comprising

a) culturing the host cell of Claim 20 for a duration of time under conditions suitable for expression of OxyR transcriptional regulator protein; and

b) collecting the OxyR transcriptional regulator protein.

27. (Currently Amended) A *Coryneform* bacterium, which comprises an overexpressed polynucleotide which comprises SEQ ID NO:1, an overexpressed polynucleotide which encodes SEQ ID NO:2, or an overexpressed polynucleotide which comprises a nucleotide sequence that is at least 70% identical to SEQ ID NO:1 and encodes a protein with OxyR transcriptional regulation activity ~~enhanced expression of the *oxyR* gene~~.

28. (Currently Amended) The *Coryneform* bacterium of Claim 27, ~~wherein said *oxyR* gene comprises the~~ which comprises the polynucleotide sequence of SEQ ID NO:1.

29. (Original) *Corynebacterium glutamicum* DSM 13457.

30. (Withdrawn) Escherichia coli DSM 13244.

31. (Withdrawn) A process for producing L-amino acids comprising culturing a bacterial cell in a medium suitable for producing L-amino acids, wherein said bacterial cell comprises enhanced expression of the oxyR gene.

32. (Withdrawn) The process of Claim 31, wherein said bacterial cell is a Coryneform bacterium or Brevibacterim.

33. (Withdrawn) The process of Claim 32, wherein said bacterial cell is selected from the group consisting of Coryneform glutamicum, Corynebacterium acetoglutamicum, Corynebacterium acetoacidophilum, Corynebacterium melassecola, Corynebacterium thermoaminogenes, Brevibacterium flavum, Brevibacterium lactofermentum, and Brevibacterium divaricatum.

34. (Withdrawn) The process of Claim 31, wherein said oxyR gene comprises the polynucleotide sequence of SEQ ID NO:1.

35. (Withdrawn) The process of Claim 31, wherein said L-amino acid is L-lysine.

36. (Withdrawn) The process of Claim 31, wherein said bacteria further comprises at least one gene whose expression is enhanced, wherein said gene is selected from the group consisting of dapA, gap, tpi, pgk, pyc, lysC, lysE, mqo, zwf, gnd, sod, and zwa1.

37. (Withdrawn) The process of Claim 32, wherein said bacteria further comprises at least one gene whose expression is attenuated, wherein said gene is selected from the group consisting of pck, pgi, poxB, and zwa2.

38. (Withdrawn) An isolated polypeptide comprising the amino acid sequence of SEQ ID NO:2.